

Amendments to the Specification:

Please replace the paragraph beginning on page 3, line 18 with the following amended paragraph:

Fig. 1. (A) Design of a 4L tiled array. Each position in the target sequence (upper case) (SEQ ID NO:12) is queried by a set of 4 probes on the chip (lower case), identical except at a single position, termed the substitution position, which is either A, C, G, or T (blue indicates complementarity, red a mismatch). Two sets of probes are shown, querying adjacent positions in the target (SEQ ID NOS:13-20). (B) Effect of change in the target sequence. The probes are the same as in panel A, but the target now contains a single base substitution (C, shown in green) (SEQ ID NO:21). The probe set querying the changed base still has a perfect match (the G probe). However, probes in adjacent sets that overlap the altered target position (SEQ ID NOS:22-29) now have either one or two mismatches (red), instead of zero or one, since they were designed to match the target shown in panel A. (C) Hybridization to a 4L tiled array and detection of a base change in the target. The array shown was designed to the mt1 sequence. (Upper panel) hybridization to mt1 (SEQ ID NO:12). The substitution used in each row of probes is indicated to the left of the image. The target sequence can be read 5' to 3' from left to right as the complement of the substitution base with the brightest signal. With hybridization to mt2 (lower panel) (SEQ ID NO:21), which differs from mt1 in this region by a T → C transition, the G probe at position 16,493 is now a perfect match, with the other three probes having single base mismatches (A 5, C 3, G 37, T 4 counts). However, at flanking positions, the probes have either single or double base mismatches, since the mt2 transition now occurs away from the query position.